



SEQUENCE LISTING

<110> Korman, Allen  
Halk, Edward L.  
Lonberg, Nils  
Medarex, Inc.

<120> Human CTLA-4 Antibodies and Their Uses

<130> 014643-010510US

<140> US 09/644,668

<141> 2000-08-24

<150> US 60/150,452

<151> 1999-08-24

<160> 41

<170> PatentIn Ver. 2.1

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<213> Artificial Sequence

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<223> Description of Artificial Sequence:cloning vector  
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<211> 349

<212> DNA

<213> Homo sapiens

<220>

<223> preliminary sequence for heavy chain fragment  
10D1.3

<400> 2

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attcaccatc tccagagaca attccaagaa cacgctgtat ctgcaaatga acagcctgag 240
agctgaggac acggctatat attactgtgc gaggaccggc tggctggggc cttttgacta 300
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<211> 321

<212> DNA

<213> Homo sapiens

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<223> preliminary sequence for light chain fragment  
10D1.3

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tctcatcta tggtgcatc agcagggcca ctggcatccc agacagggtc agtggcagtg 180
ggctcgggac agacttcact ctcaccatca gcagactgga gcctgaagat tttgcagtgt 240
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<210> 4  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> Vk A-27 germline sequence

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 cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
 gacagggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
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<210> 5  
 <211> 95  
 <212> PRT  
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<220>  
 <223> light chain variable region predicted sequence for  
 Vk A-27 germline

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 20 25 30  
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
 35 40 45  
 Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
 50 55 60  
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
 65 70 75 80  
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser  
 85 90 95

<210> 6  
 <211> 325  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> light chain variable region (Vk), 10D1 from Vk  
 A-27

<400> 6  
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 cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
 gacagggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
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 caagggacca aggtggaaat caaac 325

<210> 7  
 <211> 108  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> light chain variable region predicted sequence for  
 10D1 from Vk A-27

<400> 7  
 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly  
           1                  5                  10                  15  
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser  
                   20                  25                  30  
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
           35                  40                  45  
 Ile Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
           50                  55                  60  
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
           65                  70                  75                  80  
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
                   85                  90                  95  
 Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
           100                  105

<210> 8  
 <211> 325  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> light chain variable region (Vk) 4B6 from Vk A-27

<400> 8  
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 cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
 gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
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<210> 9  
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 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> light chain variable region predicted sequence for  
 4B6 from Vk A-27

<400> 9

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly  
 1 5 10 15  
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser  
 20 25 30  
 Phe Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
 35 40 45  
 Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
 50 55 60  
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
 65 70 75 80  
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
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 Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
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<210> 10  
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 <213> Homo sapiens

<220>  
 <223> Vk L-15 germline sequence

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 gagaaagccc ctaagtcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180  
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 gaagattttg caacttatta ctgccaacag tataatagtt accctcc 287

<210> 11  
 <211> 94  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> light chain variable region predicted sequence for  
 Vk L-15 germline

<400> 11  
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
 1 5 10 15  
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp  
 20 25 30  
 Leu Ala Trp Tyr Gln Gln Lys Pro Glu Lys Ala Pro Lys Ser Leu Ile  
 35 40 45  
 Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60  
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65

70

75

80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr  
                   85                                  90

&lt;210&gt; 12

&lt;211&gt; 322

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;223&gt; light chain variable region Vk 1E2 from Vk L-15

&lt;400&gt; 12

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 gagaaagccc ctaagtcctt gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180  
 aggttcagcg gcagtggatc tgggacagat ttactctca ccatcagcag cctgcagcct 240  
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 gggaccaagg tggaaatcaa ac 322

&lt;210&gt; 13

&lt;211&gt; 107

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

<223> light chain variable region predicted sequence for  
 1E2 from Vk L-15

&lt;400&gt; 13

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
   1                  5                          10                          15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp  
                   20                          25                          30

Leu Ala Trp Tyr Gln Gln Lys Pro Glu Lys Ala Pro Lys Ser Leu Ile  
                   35                          40                          45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly  
                   50                          55                          60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
   65                          70                          75                          80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Pro  
                   85                          90                          95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
                   100                          105

&lt;210&gt; 14

&lt;211&gt; 294

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

<223> VH 3-30.3 germline sequence

<400> 14

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ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagcaa taaatactac 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
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<210> 15

<211> 98

<212> PRT

<213> Homo sapiens

<220>

<223> heavy chain variable region predicted sequence for  
VH 3-30.3 germline

<400> 15

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Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
  1                      5                      10                      15
```

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
          20                      25                      30
```

```
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
      35                      40                      45
```

```
Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
      50                      55                      60
```

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
      65                      70                      75                      80
```

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Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
          85                      90                      95
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Ala Arg

<210> 16

<211> 355

<212> DNA

<213> Homo sapiens

<220>

<223> heavy chain variable region VH 10D1 from VH 3-30.3

<400> 16

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<210> 17

<211> 118

<212> PRT

<213> Homo sapiens

<220>

<223> heavy chain variable region predicted sequence for  
10D1 from VH 3-30.3

<400> 17

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Thr Phe Ile Ser Tyr Asp Gly Asn Asn Lys Tyr Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys  
85 90 95

Ala Arg Thr Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr  
100 105 110

Leu Val Thr Val Ser Ser  
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<210> 18

<211> 355

<212> DNA

<213> Homo sapiens

<220>

<223> heavy chain variable region VH 4B6 from VH 3-30.3

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<210> 19

<211> 118

<212> PRT

<213> Homo sapiens

<220>

<223> heavy chain variable region predicted sequence for  
4B6 from VH 3-30.3

<400> 19

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg



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      1             5             10             15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
      20             25             30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
      35             40             45
Thr Phe Ile Ser Tyr Asp Gly Ser Asn Lys His Tyr Ala Asp Ser Val
      50             55             60
Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
      65             70             75             80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys
      85             90             95
Ala Arg Thr Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr
      100            105            110
Leu Val Thr Val Ser Ser
      115

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<210> 20

<211> 296

<212> DNA

<213> Homo sapiens

<220>

<223> VH 3-33 germline sequence

<400> 20

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<210> 21

<211> 98

<212> PRT

<213> Homo sapiens

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<223> heavy chain variable region predicted sequence for  
VH 3-33 germline

<400> 21

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      20             25             30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
      35             40             45
Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
      50             55             60

```

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg

<210> 22  
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<212> DNA  
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<220>  
<223> heavy chain variable region VH 1E2 from VH 3-33

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ccaggcaagg ggctggagtg ggtggcagtt atatggtatg atggaagtaa taaatactat 180  
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240  
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<210> 23  
<211> 119  
<212> PRT  
<213> Homo sapiens

<220>  
<223> heavy chain variable region predicted sequence for  
1E2 from VH 3-33

<400> 23  
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

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&lt;400&gt; 29

Gly Ala Phe Ser Arg Ala Thr

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&lt;211&gt; 7

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;223&gt; light chain CDR2 (HuMab 4B6)

&lt;400&gt; 30

Gly Ala Ser Ser Arg Ala Thr

1 5

&lt;210&gt; 31

&lt;211&gt; 7

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;223&gt; light chain CDR2 (HuMab 1E2)

&lt;400&gt; 31

Ala Ala Ser Ser Leu Gln Ser

1 5

&lt;210&gt; 32

&lt;211&gt; 17

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

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&lt;223&gt; heavy chain CDR2 (HuMab 10D1)

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Phe Ile Ser Tyr Asp Gly Asn Asn Lys Tyr Tyr Ala Asp Ser Val Lys

1 5 10 15

Gly

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Gly

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<400> 34  
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<223> Description of Artificial Sequence:kappa light  
chain plasmid pCK7-96 (partial)

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